SEQUENCE LISTING

<110> Cox III, George Norbert
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Spratt, Sharon Kaye
Sangamo Biosciences, Inc.

<120> Regulation of Endogenous Gene Expression in Cells Using Zinc Finger Proteins

<130> 019496-002200US

<140> 09/229,037
<141> 1999-01-12

<160> 40

<170> PatentIn Ver. 2.0

<210> 1
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:exemplary motif of C2H2 class of zinc finger proteins (ZFP)

<220>
<221> MOD_RES
<222> (2)..(3)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (4)..(5)
<223> Xaa = any amino acid, may be present or absent

<220>
<221> MOD_RES
<222> (7)..(18)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (20)..(22)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (23)..(24)
<223> Xaa = any amino acid, may be present or absent

<400> 1
Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa His Xaa Xaa Xaa Xaa Xaa His
20 25

<210> 2
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ZFP target site
with two overlapping D-able subsites

<220>
<221> modified_base
<222> (1)..(2)
<223> n = g,a,c or t

<220>
<221> modified_base
<222> (5)
<223> n = g,a,c or t

<220>
<221> modified_base
<222> (8)
<223> n = g,a,c or t

<220>
<221> modified_base
<222> (9)
<223> n = a,c or t; if g, then position 10 cannot be g
or t

<220>
<221> modified_base
<222> (10)
<223> n = a or c; if g or t, then position 9 cannot be g

<400> 2
nngkngknnn 10

<210> 3
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ZFP target site
with three overlapping D-able subsites

<220>
<221> modified_base
<222> (1)..(2)
<223> n = g,a,c or t

<220>
<221> modified_base
<222> (5)
<223> n = g,a,c or t

<220>
<221> modified_base
<222> (8)
<223> n = g,a,c or t

<400> 3
nngkngkngk 10

<210> 4
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:linker

<400> 4
Asp Gly Gly Gly Ser
1 5

<210> 5
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:linker

<400> 5
Thr Gly Glu Lys Pro
1 5

<210> 6
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:linker

<400> 6
Leu Arg Gln Lys Asp Gly Glu Arg Pro
1 5

<210> 7
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:linker

<400> 7
Gly Gly Arg Arg
1

<210> 8
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:linker

<400> 8
Gly Gly Gly Gly Ser
1 5

<210> 9
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:linker

<400> 9
Gly Gly Arg Arg Gly Gly Gly Ser
1 5

<210> 10
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:linker

<400> 10
Leu Arg Gln Arg Asp Gly Glu Arg Pro
1 5

<210> 11
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:linker

<400> 11
Leu Arg Gln Lys Asp Gly Gly Gly Ser Glu Arg Pro
1 5 10

<210> 12
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:linker

<400> 12
Leu Arg Gln Lys Asp Gly Gly Gly Ser Gly Gly Gly Ser Glu Arg Pro
1 5 10 15

<210> 13
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ZFP target site region surrounding initiation site of vascular endothelial growth factor (VEGF) gene containing two 9-base pair target sites

<220>
<221> protein_bind
<222> (4)..(12)
<223> upstream 9-base pair ZFP VEGF1 target site

<220>
<221> protein_bind
<222> (14)..(22)
<223> downstream 9-base pair ZFP VEGF3a target site

<400> 13
agcggggagg atcgcggagg cttgg 25

<210> 14
<211> 298
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:VEGF1 ZFP construct targeting upstream 9-base pair target site in VEGF promoter

<220>
<221> CDS
<222> (2)..(298)
<223> VEGF1

<400> 14
g gta ccc ata cct ggc aag aag aag cag cac atc tgc cac atc cag ggc 49
Val Pro Ile Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly
1 5 10 15

tgt ggt aaa gtt tac ggc aca acc tca aat ctg cgt cgt cac ctg cgc 97
Cys Gly Lys Val Tyr Gly Thr Thr Ser Asn Leu Arg Arg His Leu Arg
20 25 30

tgg cac acc ggc gag agg cct ttc atg tgt acc tgg tcc tac tgt ggt 145
Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly
35 40 45

aaa cgc ttc acc cgt tcg tca aac ctg cag cgt cac aag cgt acc cac 193
Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr His
50 55 60

```
acc ggt gag aag aaa ttt gct tgc ccg gag tgt ccg aag cgc ttc atg   241
Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met
 65                  70                  75                  80

cgt agt gac cac ctg tcc cgt cac atc aag acc cac cag aat aag aag   289
Arg Ser Asp His Leu Ser Arg His Ile Lys Thr His Gln Asn Lys Lys
                85                  90                  95

ggt gga tcc                                                      298
Gly Gly Ser
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<210> 15
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:VEGF1 ZFP construct targeting upstream 9-base pair target site in VEGF promoter

<400> 15

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Val Pro Ile Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly
  1               5                  10                  15

Cys Gly Lys Val Tyr Gly Thr Thr Ser Asn Leu Arg Arg His Leu Arg
             20                  25                  30

Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly
         35                  40                  45

Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr His
     50                  55                  60

Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met
 65                  70                  75                  80

Arg Ser Asp His Leu Ser Arg His Ile Lys Thr His Gln Asn Lys Lys
                85                  90                  95

Gly Gly Ser
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<210> 16
<211> 298
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:VEGF3a ZFP construct targeting downstream 9-base pair target site in VEGF promoter

<220>
<221> CDS
<222> (2)..(298)
<223> VEGF3a

<400> 16
g gta ccc ata cct ggc aag aag aag cag cac atc tgc cac atc cag ggc 49
Val Pro Ile Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly
1 5 10 15

tgt ggt aaa gtt tac ggc cag tcc tcc gac ctg cag cgt cac ctg cgc 97
Cys Gly Lys Val Tyr Gly Gln Ser Ser Asp Leu Gln Arg His Leu Arg
20 25 30

tgg cac acc ggc gag agg cct ttc atg tgt acc tgg tcc tac tgt ggt 145
Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly
35 40 45

aaa cgc ttc acc cgt tcg tca aac cta cag agg cac aag cgt aca cac 193
Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr His
50 55 60

acc ggt gag aag aaa ttt gct tgc ccg gag tgt ccg aag cgc ttc atg 241
Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met
65 70 75 80

cga agt gac gag ctg tca cga cat atc aag acc cac cag aac aag aag 289
Arg Ser Asp Glu Leu Ser Arg His Ile Lys Thr His Gln Asn Lys Lys
85 90 95

ggt gga tcc 298
Gly Gly Ser

<210> 17
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:VEGF3a ZFP
construct targeting downstream 9-base pair target
site in VEGF promoter

<400> 17
Val Pro Ile Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly
1 5 10 15

Cys Gly Lys Val Tyr Gly Gln Ser Ser Asp Leu Gln Arg His Leu Arg
20 25 30

Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly
35 40 45

Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr His
50 55 60

Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met
65 70 75 80

Arg Ser Asp Glu Leu Ser Arg His Ile Lys Thr His Gln Asn Lys Lys
85 90 95

Gly Gly Ser

<210> 18
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:VEGF DNA target site 1 recognition (top) strand

<220>
<221> protein_bind
<222> (11)..(19)
<223> VEGF DNA ZFP target site 1

<400> 18
catgcatagc ggggaggatc gccatcgat 29

<210> 19
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:VEGF DNA site 1 complementary (bottom) strand

<400> 19
atcgatggcg atcctccccg ctatgcatg 29

<210> 20
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:VEGF DNA target site 3 recognition (top) strand

<220>
<221> protein_bind
<222> (11)..(19)
<223> VEGF DNA ZFP target site 3

<400> 20
catgcatatc gcggaggctt ggcatcgat 29

<210> 21
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:VEGF DNA target site 3 complementary (bottom) strand

<400> 21
atcgatgcca agcctccgcg atatgcatg 29

<210> 22
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SPE7

<400> 22
gagcagaatt cggcaagaag aagcagcac 29

<210> 23
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SPEamp12

<400> 23
gtggtctaga cagctcgtca cttcgc 26

<210> 24
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SPE
amp13

<400> 24
ggagccaagg ctgtggtaaa gtttacgg 28

<210> 25
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SPEamp11

<400> 25
ggagaagctt ggatcctcat tatccc 26

<210> 26
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:sequence
ligated between XbaI and StyI sites

<400> 26
tctagacaca tcaaaaccca ccagaacaag aaagacggcg gtggcagcgg caaaaagaaa 60

cagcacatat gtcacatcca agg 83

<210> 27
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer GB19

<400> 27
gccatgccgg tacccatacc tggcaagaag aagcagcac 39

<210> 28
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer GB10

<400> 28
cagatcggat ccacccttct tattctggtg ggt 33

<210> 29
<211> 589
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:designed
6-finger ZFP VEGF3a/1 from KpnI to BamHI

<220>
<221> CDS
<222> (2)..(589)
<223> VEGF3a/1

<400> 29
g gta ccc ata cct ggc aag aag aag cag cac atc tgc cac atc cag ggc 49
Val Pro Ile Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly
1 5 10 15

tgt ggt aaa gtt tac ggc cag tcc tcc gac ctg cag cgt cac ctg cgc 97
Cys Gly Lys Val Tyr Gly Gln Ser Ser Asp Leu Gln Arg His Leu Arg
20 25 30

tgg cac acc ggc gag agg cct ttc atg tgt acc tgg tcc tac tgt ggt 145
Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly
35 40 45

aaa cgc ttc aca cgt tcg tca aac cta cag agg cac aag cgt aca cac 193
Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr His
50 55 60

```
aca ggt gag aag aaa ttt gct tgc ccg gag tgt ccg aag cgc ttc atg   241
Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met
 65                  70                  75                  80

cga agt gac gag ctg tct aga cac atc aaa acc cac cag aac aag aaa   289
Arg Ser Asp Glu Leu Ser Arg His Ile Lys Thr His Gln Asn Lys Lys
                85                  90                  95

gac ggc ggt ggc agc ggc aaa aag aaa cag cac ata tgt cac atc caa   337
Asp Gly Gly Gly Ser Gly Lys Lys Lys Gln His Ile Cys His Ile Gln
            100                 105                 110

ggc tgt ggt aaa gtt tac ggc aca acc tca aat ctg cgt cgt cac ctg   385
Gly Cys Gly Lys Val Tyr Gly Thr Thr Ser Asn Leu Arg Arg His Leu
        115                 120                 125

cgc tgg cac acc ggc gag agg cct ttc atg tgt acc tgg tcc tac tgt   433
Arg Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys
    130                 135                 140

ggt aaa cgc ttc acc cgt tcg tca aac ctg cag cgt cac aag cgt acc   481
Gly Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr
145                 150                 155                 160

cac acc ggt gag aag aaa ttt gct tgc ccg gag tgt ccg aag cgc ttc   529
His Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe
                165                 170                 175

atg cgt agt gac cac ctg tcc cgt cac atc aag acc cac cag aat aag   577
Met Arg Ser Asp His Leu Ser Arg His Ile Lys Thr His Gln Asn Lys
            180                 185                 190

aag ggt gga tcc                                                  589
Lys Gly Gly Ser
        195
```

<210> 30
<211> 196
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:designed
6-finger ZFP VEGF3a/1 from KpnI to BamHI

<400> 30

```
Val Pro Ile Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly
  1               5                  10                  15

Cys Gly Lys Val Tyr Gly Gln Ser Ser Asp Leu Gln Arg His Leu Arg
            20                  25                  30

Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly
        35                  40                  45

Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr His
    50                  55                  60

Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met
65                  70                  75                  80
```

Arg Ser Asp Glu Leu Ser Arg His Ile Lys Thr His Gln Asn Lys Lys
85 90 95

Asp Gly Gly Gly Ser Gly Lys Lys Lys Gln His Ile Cys His Ile Gln
100 105 110

Gly Cys Gly Lys Val Tyr Gly Thr Thr Ser Asn Leu Arg Arg His Leu
115 120 125

Arg Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys
130 135 140

Gly Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr
145 150 155 160

His Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe
165 170 175

Met Arg Ser Asp His Leu Ser Arg His Ile Lys Thr His Gln Asn Lys
180 185 190

Lys Gly Gly Ser
195

<210> 31
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:JVF9 VEGF3a/1
target oligonucleotide

<400> 31
agcgagcggg gaggatcgcg gaggcttggg gcagccgggt ag 42

<210> 32
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:JVF10 VEGF3a/1
target oligonucleotide complementary sequence

<400> 32
cgctctaccc ggctgcccca agcctccgcg atcctccccg ct 42

<210> 33
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer JVF24

<400> 33
cgcggatccg ccccccccgac cgatg 25

<210> 34
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:downstream primer JVF25

<400> 34
ccgcaagctt acttgtcatc gtcgtccttg tagtcgctgc ccccaccgta ctcgtcaatt 60

cc 62

<210> 35
<211> 7
<212> PRT
<213> Simian virus 40

<220>
<221> PEPTIDE
<222> (1)..(7)
<223> SV40 large T antigen nuclear localization sequence (NLS)

<400> 35
Pro Lys Lys Lys Arg Lys Val
1 5

<210> 36
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:segment from EcoRI to KpnI containing Kozak sequence including initiation codon and SV40 NLS

<400> 36
gaattcgcta gcgccaccat ggcccccaag aagaagagga aggtgggaat ccatggggta 60

c 61

<210> 37
<211> 187
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:segment from KpnI to XhoI containing BamHI site, KRAB-A box from KOX1, FLAG epitope and HindIII site

<400> 37
ggtacccggg gatcccggac actggtgacc ttcaaggatg tatttgtgga cttcaccagg 60

gaggagtgga agctgctgga cactgctcag cagatcgtgt acagaaatgt gatgctggag 120

aactataaga acctggtttc cttgggcagc gactacaagg acgacgatga caagtaagct 180

tctcgag 187

<210> 38
<211> 277
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:inserted
fragment from BamHI to HindIII sites

<400> 38
ggatccgccc ccccgaccga tgtcagcctg ggggacgagc tccacttaga cggcgaggac 60

gtggcgatgg cgcatgccga cgcgctagac gatttcgatc tggacatgtt gggggacggg 120

gattccccgg ggccgggatt taccccccac gactccgccc cctacggcgc tctggatatg 180

gccgacttcg agtttgagca gatgtttacc gatgcccttg gaattgacga gtacggtggg 240

ggcagcgact acaaggacga cgatgacaag taagctt 277

<210> 39
<211> 118
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:sequence
replacing NLS-KRAB-FLAG with NLS-FLAG only

<400> 39
gaattcgcta gcgccaccat ggcccccaag aagaagagga aggtgggaat ccatggggta 60

cccggggatg gatccggcag cgactacaag gacgacgatg acaagtaagc ttctcgag 118

<210> 40
<211> 204
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:insert into
MluI/BglII sites of pGL3-Control to create
pVFR1-4x

<400> 40
acgcgtaagc ttgctagcga gcggggagga tcgcggaggc ttggggcagc cgggtagagc 60

gagcggggag gatcgcggag gcttggggca gccgggtaga gcgagcgggg aggatcgcgg 120

aggcttgggg cagccgggta gagcgagcgg ggaggatcgc ggaggcttgg ggcagccggg 180

tagagcgctc agaagcttag atct 204